



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of:  
Tormo *et al.*

Serial No.: Not Assigned

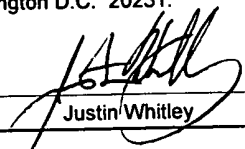
Filed: Concurrently

For: INHIBITION OF Bcl-2 PROTEIN  
EXPRESSION BY LIPOSOMAL  
ANTISENSE  
OLIGODEOXYNUCLEOTIDES

Group Art Unit: Not Assigned

Examiner: Not Assigned

Atty. Dkt. No.: UTXC:504/WIM

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I hereby certify that this paper or fee is being deposited with the United States Postal Service "EXPRESS MAIL POST OFFICE TO ADDRESSEE" service under 37 C.F.R. 1.10 on the date indicated above and is addressed to: Assistant Commissioner for Patents, Washington D.C. 20231.	
 Justin Whitley	

STATEMENT AS REQUIRED UNDER 37 C.F.R. § 1.821(f)

ATTN: PATENT APPLICATIONS

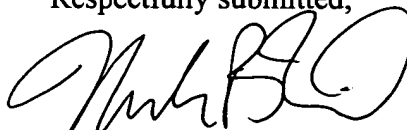
Assistant Commissioner for Patents  
Washington, D.C. 20231

Sir:

Submitted herewith is a computer readable form of the sequence listing and a paper copy of the sequence listing of those sequences in the captioned patent application. The computer readable form of the sequence listing is the same as the paper copy of the sequence listing. The

sequence information provided in the Specification is also the same as the sequence listing of the enclosed computer readable and paper forms of the sequence.

Respectfully submitted,



Mark B. Wilson  
Reg. No. 37,259  
Attorney for Applicants

ARNOLD, WHITE & DURKEE  
P.O. Box 4433  
Houston, Texas 77210-4433  
(512) 418-3000

Date: October 4, 1996



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Tormo, Mar  
Tari, Ana M.  
Lopez-Berestein, Gabriel

(ii) TITLE OF INVENTION: INHIBITION OF Bcl-2 PROTEIN EXPRESSION BY  
LIPOSOMAL ANTISENSE OLIGODEOXYNUCLEOTIDES

(iii) NUMBER OF SEQUENCES: 7

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Arnold, White & Durkee  
(B) STREET: P.O. Box 4433  
(C) CITY: Houston  
(D) STATE: Texas  
(E) COUNTRY: United States of America  
(F) ZIP: 77210

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US Unknown  
(B) FILING DATE: Concurrently Herewith  
(C) CLASSIFICATION: Unknown

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wilson, Mark B.  
(B) REGISTRATION NUMBER: 37,259  
(C) REFERENCE/DOCKET NUMBER: UTXC:504

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (512) 418-3000  
(B) TELEFAX: (512) 474-7577

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGCGTGCGC CATCCTTC

18

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACGGTCCGCC ACTCCTTCCC

20

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTGAAGGGCT TCTTCC

16

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5086 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1459..2175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCGCCCGCCC CTCCGCGCCG CCTGCCCCGCC CGCCCGCCGC GCTCCCGCCC GCCGCTCTCC	60
GTGGCCCCGC CGCGCTGCCG CCGCCGCCGC TGCCAGCGAA GGTGCCGGGG CTCCGGGCCC	120
TCCCTGCCGG CGGCCGTCAG CGCTCGGAGC GAACTGCGCG ACGGGAGGTC CGGGAGGCGA	180
CCGTAGTCGC GCCGCCGCGC AGGACCAGGA GGAGGAGAAA GGGTGCGCAG CCCGGAGGCG	240
GGGTGCGCCG GTGGGGTGCA GCGGAAGAGG GGGTCCAGGG GGGAGAACTT CGTAGCAGTC	300
ATCCTTTTTA GGAAAAGAGG GAAAAAATAA AACCCTCCCC CACCACCTCC TTCTCCCCAC	360
CCCTCGCCGC ACCACACACA GCGCGGGCTT CTAGCGCTCG GCACCGGCGG GCCAGGCGCG	420
TCCTGCCTTC ATTTATCCAG CAGCTTTTCG GAAAATGCAT TTGCTGTTCG GAGTTTAATC	480
AGAAGACGAT TCCTGCCTCC GTCCCCGGCT CCTTCATCGT CCCATCTCCC CTGTCTCTCT	540
CCTGGGGAGG CGTGAAGCGG TCCCGTGGAT AGAGATTCAT GCCTGTGTCC GCGCGTGTGT	600
GCGCGCGTAT AAATTGCCGA GAAGGGGAAA ACATCACAGG ACTTCTGCGA ATACCGGACT	660
GAAAATTGTA ATTCATCTGC CGCCGCCGCT GCCAAAAAAA AACTCGAGCT CTTGAGATCT	720

CCGGTTGGGA TTCCTGCGGA TTGACATTTC TGTGAAGCAG AAGTCTGGGA ATCGATCTGG	780
AAATCCTCCT AATTTTACT CCCTCTCCCC CCGACTCCTG ATTCATTGGG AAGTTTCAAA	840
TCAGCTATAA CTGGAGAGTG CTGAAGATTG ATGGGATCGT TGCCTTATGC ATTTGTTTTG	900
GTTTTACAAA AAGGAACTT GACAGAGGAT CATGCTGTAC TTAAAAATA CAAGTAAGTC	960
TCGCACAGGA AATTGGTTTA ATGTAACTTT CAATGGAAAC CTTTGAGATT TTTTACTTAA	1020
AGTGCATTCG AGTAAATTTA ATTTCCAGGC AGCTTAATAC ATTGTTTTTA GCCGTGTTAC	1080
TTGTAGTGTG TATGCCCTGC TTTCACCTCAG TGTGTACAGG GAAACGCACC TGATTTTTTA	1140
CTTATTAGTT TGTTTTTCT TTAACCTTTC AGCATCACAG AGGAAGTAGA CTGATATTAA	1200
CAATACTTAC TAATAATAAC GTGCCTCATG AAATAAAGAT CCGAAAGGAA TTGGAATAAA	1260
AATTCCTGC GTCTCATGCC AAGAGGGAAA CACCAGAATC AAGTGTTCCG CGTGATTGAA	1320
GACACCCCCT CGTCCAAGAA TGCAAAGCAC ATCCAATAAA ATAGCTGGAT TATAACTCCT	1380
CTTCTTTCTC TGGGGGCCGT GGGGTGGGAG CTGGGGCGAG AGGTGCCGTT GGCCCCCGTT	1440
GCTTTTCCTC TGGGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC GAC AAC	1491
Met Ala His Ala Gly Arg Thr Gly Tyr Asp Asn	
1 5 10	
CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG AGG GGC	1539
Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln Arg Gly	
15 20 25	
TAC GAG TGG GAT GCG GGA GAT GTG GGC GCC GCG CCC CCG GGG GCC GCC	1587
Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly Ala Ala	
30 35 40	
CCC GCA CCG GGC ATC TTC TCC TCC CAG CCC GGG CAC ACG CCC CAT CCA	1635
Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro His Pro	
45 50 55	
GCC GCA TCC CGC GAC CCG GTC GCC AGG ACC TCG CCG CTG CAG ACC CCG	1683
Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln Thr Pro	
60 65 70 75	
GCT GCC CCC GGC GCC GCC GCG GGG CCT GCG CTC AGC CCG GTG CCA CCT	1731
Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val Pro Pro	
80 85 90	
GTG GTC CAC CTG GCC CTC CGC CAA GCC GGC GAC GAC TTC TCC CGC CGC	1779
Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser Arg Arg	
95 100 105	
TAC CGC GGC GAC TTC GCC GAG ATG TCC AGC CAG CTG CAC CTG ACG CCC	1827
Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu Thr Pro	
110 115 120	
TTC ACC GCG CGG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC TTC AGG	1875
Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu Phe Arg	
125 130 135	

GAC Asp 140	GGG Gly	GTG Val	AAC Asn	TGG Trp	GGG Gly 145	AGG Arg	ATT Ile	GTG Val	GCC Ala	TTC Phe 150	TTT Phe	GAG Glu	TTC Phe	GGT Gly	GGG Gly 155	1923
GTC Val	ATG Met	TGT Cys	GTG Val	GAG Glu 160	AGC Ser	GTC Val	AAC Asn	CGG Arg	GAG Glu 165	ATG Met	TCG Ser	CCC Pro	CTG Leu	GTG Val 170	GAC Asp	1971
AAC Asn	ATC Ile	GCC Ala	CTG Leu 175	TGG Trp	ATG Met	ACT Thr	GAG Glu 180	TAC Tyr	CTG Leu	AAC Asn	CGG Arg	CAC His	CTG Leu 185	CAC His	ACC Thr	2019
TGG Trp	ATC Ile	CAG Gln 190	GAT Asp	AAC Asn	GGA Gly	GGC Gly	TGG Trp 195	GAT Asp	GCC Ala	TTT Phe	GTG Val	GAA Glu 200	CTG Leu	TAC Tyr	GGC Gly	2067
CCC Pro	AGC Ser 205	ATG Met	CGG Arg	CCT Pro	CTG Leu	TTT Phe 210	GAT Asp	TTC Phe	TCC Ser	TGG Trp 215	CTG Leu	TCT Ser	CTG Leu	AAG Lys	ACT Thr	2115
CTG Leu 220	CTC Leu	AGT Ser	TTG Leu	GCC Ala 225	CTG Leu 225	GTG Val	GGA Gly	GCT Ala	TGC Cys	ATC Ile 230	ACC Thr	CTG Leu	GGT Gly	GCC Ala 235	TAT Tyr 235	2163
CTG Leu	AGC Ser	CAC His	AAG Lys	TGAAGTCAAC	ATGCCTGCCC	CAAACAAATA	TGCAAAAGGT									2215
TCACTAAAGC AGTAGAAATA ATATGCATTG TCAGTGATGT ACCATGAAAC AAAGCTGCAG																2275
GCTGTTTAAAG AAAAAATAAC ACACATATAA ACATCACACA CACAGACAGA CACACACACA																2335
CACAACAATT AACAGTCTTC AGGCAAAACG TCGAATCAGC TATTTACTGC CAAAGGGAAA																2395
TATCATTTAT TTTTACATT ATTAAGAAAA AAGATTTATT TATTTAAGAC AGTCCCATCA																2455
AAACTCCGTC TTTGGAAATC CGACCACTAA TTGCCAAACA CCGCTTCGTG TGGCTCCACC																2515
TGGATGTTCT GTGCCTGTAA ACATAGATTC GCTTTCCATG TTGTTGGCCG GATCACCATC																2575
TGAAGAGCAG ACGGATGGAA AAAGGACCTG ATCATTGGGG AAGCTGGCTT TCTGGCTGCT																2635
GGAGGCTGGG GAGAAGGTGT TCATTCACTT GCATTTCTTT GCCCTGGGGG CGTGATATTA																2695
ACAGAGGGAG GGTTCCTCGTG GGGGGAAGTC CATGCCTCCC TGGCCTGAAG AAGAGACTCT																2755
TTGCATATGA CTCACATGAT GCATACCTGG TGGGAGGAAA AGAGTTGGGA ACTTCAGATG																2815
GACCTAGTAC CCACTGAGAT TTCCACGCCG AAGGACAGCG ATGGGAAAAA TGCCCTTAAA																2875
TCATAGGAAA GTATTTTTTTT AAGCTACCAA TTGTGCCGAG AAAAGCATTT TAGCAATTTA																2935
TACAATATCA TCCAGTACCT TAAACCCTGA TTGTGTATAT TCATATATTT TGGATACGCA																2995
CCCCCAACT CCAATACTG GCTCTGTCTG AGTAAGAAAC AGAATCCTCT GGAACCTGAG																3055
GAAGTGAACA TTTCGGTGAC TTCCGATCAG GAAGGCTAGA GTTACCCAGA GCATCAGGCC																3115
GCCACAAGTG CCTGCTTTTA GGAGACCGAA GTCCGCAGAA CCTACCTGTG TCCCAGCTTG																3175

GAGGCCTGGT	CCTGGAAGCTG	AGCCGGGGCCC	TCACTGGCCT	CCTCCAGGGA	TGATCAACAG	3235
GGTAGTGTGG	TCTCCGAATG	TCTGGAAGCT	GATGGATGGA	GCTCAGAAAT	CCACTGTCAA	3295
GAAAGAGCAG	TAGAGGGGTG	TGGCTGGGCC	TGTCACCCTG	GGGCCCTCCA	GGTAGGCCCCG	3355
TTTTCACGTG	GAGCATAGGA	GCCACGACCC	TTCTTAAGAC	ATGTATCACT	GTAGAGGGAA	3415
GGAACAGAGG	CCCTGGGCCT	TCCTATCAGA	AGGACATGGT	GAAGGCTGGG	AACGTGAGGA	3475
GAGGCAATGG	CCACGGCCCA	TTTTGGCTGT	AGCACATGGC	ACGTTGGCTG	TGTGGCCTTG	3535
GCCACCTGTG	AGTTTAAAGC	AAGGCTTTAA	ATGACTTTGG	AGAGGGTCAC	AAATCCTAAA	3595
AGAAGCATTG	AAGTGAGGTG	TCATGGATTA	ATTGACCCCT	GTCATATGGAA	TTACATGTAA	3655
AACATTATCT	TGTCACCTGTA	GTTTGGTTTT	ATTTGAAAAC	CTGACAAAAA	AAAAGTTCCA	3715
GGTGTGGAAT	ATGGGGGTTA	TCTGTACATC	CTGGGGCATT	AAAAAAAAAT	CAATGGTGGG	3775
GAACTATAAA	GAAGTAACAA	AAGAAGTGAC	ATCTTCAGCA	AATAAACTAG	GAAATTTTTT	3835
TTTCTTCCAG	TTTAGAATCA	GCCTTGAAAC	ATTGATGGAA	TAAGTCTGTG	GCATTATTGC	3895
ATTATATACC	ATTTATCTGT	ATTAAGTTTG	GAATGTACTC	TGTTCAATGT	TTAATGCTGT	3955
GGTTGATATT	TCGAAAGCTG	CTTTAAAAAA	ATACATGCAT	CTCAGCGTTT	TTTTGTTTTT	4015
AATTGTATTT	AGTTATGGCC	TATACACTAT	TTGTGAGCAA	AGGTGATCGT	TTTCTGTTTG	4075
AGATTTTTAT	CTCTTGATTG	TTCAAAAGCA	TTCTGAGAAG	GTGAGATAAG	CCCTGAGTCT	4135
CAGCTACCTA	AGAAAAACCT	GGATGTCACT	GGCCACTGAG	GAGCTTTGTT	TCAACCAAGT	4195
CATGTGCATT	TCCACGTCAA	CAGAATTGTT	TATTGTGACA	GTTATATCTG	TTGTCCCTTT	4255
GACCTTGTTT	CTTGAAGGTT	TCCTCGTCCC	TGGGCAATTC	CGCATTTAAT	TCATGGTATT	4315
CAGGATTACA	TGCATGTTTG	GTAAACCCCA	TGAGATTCAT	TCAGTTAAAA	ATCCAGATGG	4375
CGAATGACCA	GCAGATTCAA	ATCTATGGTG	GTTTGACCTT	TAGAGAGTTG	CTTTACGTGG	4435
CCTGTTTCAA	CACAGACCCA	CCCAGAGCCC	TCCTGCCCTC	CTTCCGCGGG	GGCTTTCTCA	4495
TGGCTGTCCT	TCAGGGTCTT	CCTGAAATGC	AGTGGTCGTT	ACGCTCCACC	AAGAAAGCAG	4555
GAAACCTGTG	GTATGAAGCC	AGACCTCCCC	GGCGGGCCTC	AGGGAACAGA	ATGATCAGAC	4615
CTTTGAATGA	TTCTAATTTT	TAAGCAAAAT	ATTATTTTAT	GAAAGGTTTA	CATTGTCAAA	4675
GTGATGAATA	TGGAATATCC	AATCCTGTGC	TGCTATCCTG	CCAAAATCAT	TTTAATGGAG	4735
TCAGTTTGCA	GTATGCTCCA	CGTGGTAAGA	TCCTCCAAGC	TGCTTTAGAA	GTAACAATGA	4795
AGAACGTGGA	CGTTTTTAAT	ATAAAGCCTG	TTTTGTCTTT	TGTTGTTGTT	CAAACGGGAT	4855
TCACAGAGTA	TTTGAAAAAT	GTATATATAT	TAAGAGGTCA	CGGGGGCTAA	TTGCTAGCTG	4915
GCTGCCTTTT	GCTGTGGGGT	TTTGTTACCT	GGTTTTAATA	ACAGTAAATG	TGCCCAGCCT	4975

CTTGCCCCCA GAACTGTACA GTATTGTGGC TGCACTTGCT CTAAGAGTAG TTGATGTTGC 5035  
 ATTTTCCTTA TTGTTAAAAA CATGTTAGAA GCAATGAATG TATATAAAAG C 5086

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 239 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Ala	His	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val	Met	1	5	10	15
Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp	Ala	20	25	30	
Gly	Asp	Val	Gly	Ala	Ala	Pro	Pro	Gly	Ala	Ala	Pro	Ala	Pro	Gly	Ile	35	40	45	
Phe	Ser	Ser	Gln	Pro	Gly	His	Thr	Pro	His	Pro	Ala	Ala	Ser	Arg	Asp	50	55	60	
Pro	Val	Ala	Arg	Thr	Ser	Pro	Leu	Gln	Thr	Pro	Ala	Ala	Pro	Gly	Ala	65	70	75	80
Ala	Ala	Gly	Pro	Ala	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Ala	85	90	95	
Leu	Arg	Gln	Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Gly	Asp	Phe	100	105	110	
Ala	Glu	Met	Ser	Ser	Gln	Leu	His	Leu	Thr	Pro	Phe	Thr	Ala	Arg	Gly	115	120	125	
Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp	130	135	140	
Gly	Arg	Ile	Val	Ala	Phe	Phe	Glu	Phe	Gly	Gly	Val	Met	Cys	Val	Glu	145	150	155	160
Ser	Val	Asn	Arg	Glu	Met	Ser	Pro	Leu	Val	Asp	Asn	Ile	Ala	Leu	Trp	165	170	175	
Met	Thr	Glu	Tyr	Leu	Asn	Arg	His	Leu	His	Thr	Trp	Ile	Gln	Asp	Asn	180	185	190	
Gly	Gly	Trp	Asp	Ala	Phe	Val	Glu	Leu	Tyr	Gly	Pro	Ser	Met	Arg	Pro	195	200	205	
Leu	Phe	Asp	Phe	Ser	Trp	Leu	Ser	Leu	Lys	Thr	Leu	Leu	Ser	Leu	Ala	210	215	220	
Leu	Val	Gly	Ala	Cys	Ile	Thr	Leu	Gly	Ala	Tyr	Leu	Ser	His	Lys					



## (2) INFORMATION FOR SEQ ID NO:6:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 911 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 147..761

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TGATTGAAGA CACCCCCTCG TCCAAGAATG CAAAGCACAT CCAATAAAAT AGCTGGATTA	60
TAACTCCTCT TCTTTCTCTG GGGGCCGTGG GGTGGGAGCT GGGGCGAGAG GTGCCGTTGG	120
CCCCCGTTGC TTTTCCTCTG GGAAGG ATG GCG CAC GCT GGG AGA ACG GGG TAC	173
Met Ala His Ala Gly Arg Thr Gly Tyr	
1 5	
GAC AAC CGG GAG ATA GTG ATG AAG TAC ATC CAT TAT AAG CTG TCG CAG	221
Asp Asn Arg Glu Ile Val Met Lys Tyr Ile His Tyr Lys Leu Ser Gln	
10 15 20 25	
AGG GGC TAC GAG TGG GAT GCG GGA GAT GTG GGC GCC GCG CCC CCG GGG	269
Arg Gly Tyr Glu Trp Asp Ala Gly Asp Val Gly Ala Ala Pro Pro Gly	
30 35 40	
GCC GCC CCC GCA CCG GGC ATC TTC TCC TCC CAG CCC GGG CAC ACG CCC	317
Ala Ala Pro Ala Pro Gly Ile Phe Ser Ser Gln Pro Gly His Thr Pro	
45 50 55	
CAT CCA GCC GCA TCC CGC GAC CCG GTC GCC AGG ACC TCG CCG CTG CAG	365
His Pro Ala Ala Ser Arg Asp Pro Val Ala Arg Thr Ser Pro Leu Gln	
60 65 70	
ACC CCG GCT GCC CCC GGC GCC GCC GCG GGG CCT GCG CTC AGC CCG GTG	413
Thr Pro Ala Ala Pro Gly Ala Ala Ala Gly Pro Ala Leu Ser Pro Val	
75 80 85	
CCA CCT GTG GTC CAC CTG GCC CTC CGC CAA GCC GGC GAC GAC TTC TCC	461
Pro Pro Val Val His Leu Ala Leu Arg Gln Ala Gly Asp Asp Phe Ser	
90 95 100 105	
CGC CGC TAC CGC GGC GAC TTC GCC GAG ATG TCC AGC CAG CTG CAC CTG	509
Arg Arg Tyr Arg Gly Asp Phe Ala Glu Met Ser Ser Gln Leu His Leu	
110 115 120	
ACG CCC TTC ACC GCG CGG GGA CGC TTT GCC ACG GTG GTG GAG GAG CTC	557
Thr Pro Phe Thr Ala Arg Gly Arg Phe Ala Thr Val Val Glu Glu Leu	
125 130 135	
TTC AGG GAC GGG GTG AAC TGG GGG AGG ATT GTG GCC TTC TTT GAG TTC	605
Phe Arg Asp Gly Val Asn Trp Gly Arg Ile Val Ala Phe Phe Glu Phe	
140 145 150	

GGT	GGG	GTC	ATG	TGT	GTG	GAG	AGC	GTC	AAC	CGG	GAG	ATG	TCG	CCC	CTG	653			
Gly	Gly	Val	Met	Cys	Val	Glu	Ser	Val	Asn	Arg	Glu	Met	Ser	Pro	Leu				
155						160					165								
GTG	GAC	AAC	ATC	GCC	CTG	TGG	ATG	ACT	GAG	TAC	CTG	AAC	CGG	CAC	CTG	701			
Val	Asp	Asn	Ile	Ala	Leu	Trp	Met	Thr	Glu	Tyr	Leu	Asn	Arg	His	Leu				
170					175					180					185				
CAC	ACC	TGG	ATC	CAG	GAT	AAC	GGA	GGC	TGG	GTA	GGT	GCA	TCT	GGT	GAT	749			
His	Thr	Trp	Ile	Gln	Asp	Asn	Gly	Gly	Trp	Val	Gly	Ala	Ser	Gly	Asp				
				190					195					200					
GTG	AGT	CTG	GGC	TGAGGCCACA				GGTCCGAGAT				CGGGGGTTGG				AGTGCGGGTG		801	
Val	Ser	Leu	Gly																
			205																
GGCTCCTGGG CAATGGGAGG CTGTGGAGCC GGC GAAATAA AATCAGAGTT GTTGCTTCCC																861			
GGCGTGTCCC TACCTCCTCC TCTGGACAAA GCGTTCACTC CCAACCTGAC																911			

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	His	Ala	Gly	Arg	Thr	Gly	Tyr	Asp	Asn	Arg	Glu	Ile	Val	Met	
1				5					10					15		
Lys	Tyr	Ile	His	Tyr	Lys	Leu	Ser	Gln	Arg	Gly	Tyr	Glu	Trp	Asp	Ala	
			20					25					30			
Gly	Asp	Val	Gly	Ala	Ala	Pro	Pro	Gly	Ala	Ala	Pro	Ala	Pro	Gly	Ile	
		35					40					45				
Phe	Ser	Ser	Gln	Pro	Gly	His	Thr	Pro	His	Pro	Ala	Ala	Ser	Arg	Asp	
	50					55					60					
Pro	Val	Ala	Arg	Thr	Ser	Pro	Leu	Gln	Thr	Pro	Ala	Ala	Pro	Gly	Ala	
	65				70					75				80		
Ala	Ala	Gly	Pro	Ala	Leu	Ser	Pro	Val	Pro	Pro	Val	Val	His	Leu	Ala	
				85					90					95		
Leu	Arg	Gln	Ala	Gly	Asp	Asp	Phe	Ser	Arg	Arg	Tyr	Arg	Gly	Asp	Phe	
		100						105					110			
Ala	Glu	Met	Ser	Ser	Gln	Leu	His	Leu	Thr	Pro	Phe	Thr	Ala	Arg	Gly	
		115					120					125				
Arg	Phe	Ala	Thr	Val	Val	Glu	Glu	Leu	Phe	Arg	Asp	Gly	Val	Asn	Trp	
		130				135					140					

Gly Arg Ile Val Ala Phe Phe Glu Phe Gly Gly Val Met Cys Val Glu  
.145 150 155 160

Ser Val Asn Arg Glu Met Ser Pro Leu Val Asp Asn Ile Ala Leu Trp  
165 170 175

Met Thr Glu Tyr Leu Asn Arg His Leu His Thr Trp Ile Gln Asp Asn  
180 185 190

Gly Gly Trp Val Gly Ala Ser Gly Asp Val Ser Leu Gly  
195 200 205